

RAW SEQUENCE LISTING

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Application Serial Number: 10/750,323

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DATE: 10/19/2004

PATENT APPLICATION: US/10/750,323

TIME: 09:18:42

Input Set : N:\Crf3\RULE60\10750323.raw.txt

Output Set: N:\CRF4\10192004\J750323.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Pulst, Stefan M

7 (ii) TITLE OF INVENTION: NUCLEIC ACID ENCODING SPINOCEREBELLAR
8 ATAXIA-2 AND PRODUCTS RELATED THERETO

10 (iii) NUMBER OF SEQUENCES: 19

12 (iv) CORRESPONDENCE ADDRESS:

13 (A) ADDRESSEE: Mueting, Raasch & Gebhardt, P.A.

14 (B) STREET: 119 North Fourth Street

15 (C) CITY: Minneapolis

16 (D) STATE: Minnesota

17 (E) COUNTRY: USA

18 (F) ZIP: 55401

20 (v) COMPUTER READABLE FORM:

21 (A) MEDIUM TYPE: Floppy disk

22 (B) COMPUTER: IBM PC compatible

23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

26 (vi) CURRENT APPLICATION DATA:

-> 27 (A) APPLICATION NUMBER: US/10/750,323

-> 28 (B) FILING DATE: 30-Dec-2003

-> 33 (C) CLASSIFICATION: 536

-> 30 (vii) PRIOR APPLICATION DATA:

31 (A) APPLICATION NUMBER: US/08/727,084

32 (B) FILING DATE: 08-OCT-1996

35 (viii) ATTORNEY/AGENT INFORMATION:

36 (A) NAME: Mueting, Ann M.

37 (B) REGISTRATION NUMBER: 33,977

38 (C) REFERENCE/DOCKET NUMBER: 232.00010101

40 (ix) TELECOMMUNICATION INFORMATION:

41 (A) TELEPHONE: 612/305-1220

42 (B) TELEFAX: 612/305-1228

46 (2) INFORMATION FOR SEQ ID NO: 1:

48 (i) SEQUENCE CHARACTERISTICS:

49 (A) LENGTH: 516 base pairs

50 (B) TYPE: nucleic acid

51 (C) STRANDEDNESS: both

52 (D) TOPOLOGY: both

54 (ii) MOLECULE TYPE: DNA (genomic)

58 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

60	TTGGTAGCAA CGGAAACGGC GGCGGCGCGT TTCGGCCCCG CTCCCGGCGG CTCCTTGGTC	60
62	TCGGCGGGCC TCCCGCCCC TCGTCGTCG TCCTTCTCCC CCTCGCCAGC CCGGGCGCCC	120
64	CTCCGGCCGC GCCAACCCGC GCCTCCCCGC TCGGCGCCCG TCGTCCCCG CCGCGTTCCG	180

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66 GCGTCTCCTT GGCGCGCCCG GCTCCCGGCT GTCCCCGCCC GCGGTGCGAG CCGGTGTATG      240
68 GGCCCTCAC CATGTCGCTG AAGCCCCAGC AGCAGCAGCA GCAGCAGCAG CAACAGCAGC      300
70 AGCAGCAACA GCAGCAGCAG CAGCAGCAGC AGCCGCGGCC CGCGGCTGCC AATGTCCGCA      360
72 AGCCCGGCGG CAGCGGCCTT CTAGCGTCGC CCGCCGCCGC GCCTTCGCCG TCCTCGTCCT      420
74 CCGTCTCCTC GTCCTCGGCC ACGGCTCCCT CCTCGGTGGT CGCGGCGACC TCCGGCGGCG      480
76 GGAGGCCCGG CCTGGGCAGG TGGGTGTCGG CACCCC      516
78 (2) INFORMATION FOR SEQ ID NO: 2:
80   (i) SEQUENCE CHARACTERISTICS:
81       (A) LENGTH: 4481 base pairs
82       (B) TYPE: nucleic acid
83       (C) STRANDEDNESS: both
84       (D) TOPOLOGY: both
86   (ii) MOLECULE TYPE: cDNA
89   (ix) FEATURE:
90       (A) NAME/KEY: CDS
91       (B) LOCATION: 163..4101
94   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
96 ACCCCCCGAGA AAGCAACCCA GCGCGCCGCC CGTCTCTCAC GTGTCCCTCC CGGCCCCGGG      60
98 GCCACCTCAC GTTCTGCTTC CGTCTGACCC CTCCGACTTC CCGTAAAGAG TCCCTATCCG      120
100 CACCTCCGCT CCCACCCGGC GCCTCGGCGC GCCCGCCCTC CG ATG CGC TCA GCG      174
101                                     Met Arg Ser Ala
102                                     1
104 GCC GCA GCT CCT CGG AGT CCC GCG GTG GCC ACC GAG TCT CGC CGC TTC      222
105 Ala Ala Ala Pro Arg Ser Pro Ala Val Ala Thr Glu Ser Arg Arg Phe
106   5          10          15          20
108 GCC GCA GCC AGG TGG CCC GGG TGG CGC TCG CTC CAG CGG CCG GCG CGG      270
109 Ala Ala Ala Arg Trp Pro Gly Trp Arg Ser Leu Gln Arg Pro Ala Arg
110          25          30          35
112 CGG AGC GGG CGG GGC GGC GGT GGC GCG GCC CCG GGA CCG TAT CCC TCC      318
113 Arg Ser Gly Arg Gly Gly Gly Gly Ala Ala Pro Gly Pro Tyr Pro Ser
114          40          45          50
116 GCC GCC CCT CCC CCG CCC GGC CCC GGC CCC CCT CCC TCC CGG CAG AGC      366
117 Ala Ala Pro Pro Pro Pro Gly Pro Gly Pro Pro Pro Ser Arg Gln Ser
118          55          60          65
120 TCG CCT CCC TCC GCC TCA GAC TGT TTT GGT AGC AAC GGC AAC GGC GGC      414
121 Ser Pro Pro Ser Ala Ser Asp Cys Phe Gly Ser Asn Gly Asn Gly Gly
122          70          75          80
124 GGC GCG TTT CGG CCC GGC TCC CGG CGG CTC CTT GGT CTC GGC GGC CCT      462
125 Gly Ala Phe Arg Pro Gly Ser Arg Arg Leu Leu Gly Leu Gly Gly Pro
126  85          90          95          100
128 CCC CGC CCC TTC GTC GTC GTC CTT CTC CCC CTC GCC AGC CCG GGC GCC      510
129 Pro Arg Pro Phe Val Val Val Leu Leu Pro Leu Ala Ser Pro Gly Ala
130          105          110          115
132 CCT CCG GCC GCG CCA ACC CGC GCC TCC CCG CTC GGC GCC CGT GCG TCC      558
133 Pro Pro Ala Ala Pro Thr Arg Ala Ser Pro Leu Gly Ala Arg Ala Ser
134          120          125          130
136 CCG CCG CGT TCC GGC GTC TCC TTG GCG CGC CCG GCT CCC GGC TGT CCC      606
137 Pro Pro Arg Ser Gly Val Ser Leu Ala Arg Pro Ala Pro Gly Cys Pro
138          135          140          145

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140	CGC	CCG	GCG	TGC	GAG	CCG	GTG	TAT	GGG	CCC	CTC	ACC	ATG	TCG	CTG	AAG	654
141	Arg	Pro	Ala	Cys	Glu	Pro	Val	Tyr	Gly	Pro	Leu	Thr	Met	Ser	Leu	Lys	
142		150					155					160					
144	CCC	CAG	CAG	CAG	CAG	CAG	CAG	CAG	CAA	CAG	CAG	CAG	CAG	CAA	CAG		702
145	Pro	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	
146	165					170					175					180	
148	CAG	CAG	CAG	CAG	CAG	CAG	CCG	CCG	CCC	GCG	GCT	GCC	AAT	GTC	CGC		750
149	Gln	Gln	Gln	Gln	Gln	Gln	Pro	Pro	Ala	Ala	Ala	Ala	Asn	Val	Arg		
150					185					190				195			
152	AAG	CCC	GGC	GGC	AGC	GGC	CTT	CTA	GCG	TCG	CCC	GCC	GCC	GCG	CCT	TCG	798
153	Lys	Pro	Gly	Gly	Ser	Gly	Leu	Leu	Ala	Ser	Pro	Ala	Ala	Ala	Pro	Ser	
154			200						205					210			
156	CCG	TCC	TCG	TCC	TCG	GTC	TCC	TCG	TCC	TCG	GCC	ACG	GCT	CCC	TCC	TCG	846
157	Pro	Ser	Ser	Ser	Ser	Val	Ser	Ser	Ser	Ser	Ala	Thr	Ala	Pro	Ser	Ser	
158			215						220					225			
160	GTG	GTC	GCG	GCG	ACC	TCC	GGC	GGC	GGG	AGG	CCC	GGC	CTG	GGC	AGA	GGT	894
161	Val	Val	Ala	Ala	Thr	Ser	Gly	Gly	Gly	Arg	Pro	Gly	Leu	Gly	Arg	Gly	
162		230					235					240					
164	CGA	AAC	AGT	AAC	AAA	GGA	CTG	CCT	CAG	TCT	ACG	ATT	TCT	TTT	GAT	GGA	942
165	Arg	Asn	Ser	Asn	Lys	Gly	Leu	Pro	Gln	Ser	Thr	Ile	Ser	Phe	Asp	Gly	
166	245				250					255						260	
168	ATC	TAT	GCA	AAT	ATG	AGG	ATG	GTT	CAT	ATA	CTT	ACA	TCA	GTT	GTT	GGC	990
169	Ile	Tyr	Ala	Asn	Met	Arg	Met	Val	His	Ile	Leu	Thr	Ser	Val	Val	Gly	
170					265					270				275			
172	TCC	AAA	TGT	GAA	GTA	CAA	GTG	AAA	AAT	GGA	GGT	ATA	TAT	GAA	GGA	GTT	1038
173	Ser	Lys	Cys	Glu	Val	Gln	Val	Lys	Asn	Gly	Gly	Ile	Tyr	Glu	Gly	Val	
174			280						285					290			
176	TTT	AAA	ACT	TAC	AGT	CCG	AAG	TGT	GAT	TTG	GTA	CTT	GAT	GCC	GCA	CAT	1086
177	Phe	Lys	Thr	Tyr	Ser	Pro	Lys	Cys	Asp	Leu	Val	Leu	Asp	Ala	Ala	His	
178			295					300					305				
180	GAG	AAA	AGT	ACA	GAA	TCC	AGT	TCG	GGG	CCG	AAA	CGT	GAA	GAA	ATA	ATG	1134
181	Glu	Lys	Ser	Thr	Glu	Ser	Ser	Ser	Gly	Pro	Lys	Arg	Glu	Glu	Ile	Met	
182		310					315					320					
184	GAG	AGT	ATT	TTG	TTC	AAA	TGT	TCA	GAC	TTT	GTT	GTG	GTA	CAG	TTT	AAA	1182
185	Glu	Ser	Ile	Leu	Phe	Lys	Cys	Ser	Asp	Phe	Val	Val	Val	Gln	Phe	Lys	
186	325				330					335						340	
188	GAT	ATG	GAC	TCC	AGT	TAT	GCA	AAA	AGA	GAT	GCT	TTT	ACT	GAC	TCT	GCT	1230
189	Asp	Met	Asp	Ser	Ser	Tyr	Ala	Lys	Arg	Asp	Ala	Phe	Thr	Asp	Ser	Ala	
190					345					350				355			
192	ATC	AGT	GCT	AAA	GTG	AAT	GGC	GAA	CAC	AAA	GAG	AAG	GAC	CTG	GAG	CCC	1278
193	Ile	Ser	Ala	Lys	Val	Asn	Gly	Glu	His	Lys	Glu	Lys	Asp	Leu	Glu	Pro	
194			360						365					370			
196	TGG	GAT	GCA	GGT	GAA	CTC	ACA	GCC	AAT	GAG	GAA	CTT	GAG	GCT	TTG	GAA	1326
197	Trp	Asp	Ala	Gly	Glu	Leu	Thr	Ala	Asn	Glu	Glu	Leu	Glu	Ala	Leu	Glu	
198			375					380					385				
200	AAT	GAC	GTA	TCT	AAT	GGA	TGG	GAT	CCC	AAT	GAT	ATG	TTT	CGA	TAT	AAT	1374
201	Asn	Asp	Val	Ser	Asn	Gly	Trp	Asp	Pro	Asn	Asp	Met	Phe	Arg	Tyr	Asn	
202		390					395					400					
204	GAA	GAA	AAT	TAT	GGT	GTA	GTG	TCT	ACG	TAT	GAT	AGC	AGT	TTA	TCT	TCG	1422

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205	Glu	Glu	Asn	Tyr	Gly	Val	Val	Ser	Thr	Tyr	Asp	Ser	Ser	Leu	Ser	Ser	
206	405					410					415					420	
208	TAT	ACA	GTG	CCC	TTA	GAA	AGA	GAT	AAC	TCA	GAA	GAA	TTT	TTA	AAA	CGG	1470
209	Tyr	Thr	Val	Pro	Leu	Glu	Arg	Asp	Asn	Ser	Glu	Glu	Phe	Leu	Lys	Arg	
210					425					430					435		
212	GAA	GCA	AGG	GCA	AAC	CAG	TTA	GCA	GAA	GAA	ATT	GAG	TCA	AGT	GCC	CAG	1518
213	Glu	Ala	Arg	Ala	Asn	Gln	Leu	Ala	Glu	Glu	Ile	Glu	Ser	Ser	Ala	Gln	
214				440						445					450		
216	TAC	AAA	GCT	CGA	GTG	GCC	CTG	GAA	AAT	GAT	GAT	AGG	AGT	GAG	GAA	GAA	1566
217	Tyr	Lys	Ala	Arg	Val	Ala	Leu	Glu	Asn	Asp	Asp	Arg	Ser	Glu	Glu	Glu	
218			455					460						465			
220	AAA	TAC	ACA	GCA	GTT	CAG	AGA	AAT	TCC	AGT	GAA	CGT	GAG	GGG	CAC	AGC	1614
221	Lys	Tyr	Thr	Ala	Val	Gln	Arg	Asn	Ser	Ser	Glu	Arg	Glu	Gly	His	Ser	
222		470					475					480					
224	ATA	AAC	ACT	AGG	GAA	AAT	AAA	TAT	ATT	CCT	CCT	GGA	CAA	AGA	AAT	AGA	1662
225	Ile	Asn	Thr	Arg	Glu	Asn	Lys	Tyr	Ile	Pro	Pro	Gly	Gln	Arg	Asn	Arg	
226	485					490					495					500	
228	GAA	GTC	ATA	TCC	TGG	GGA	AGT	GGG	AGA	CAG	AAT	TCA	CCG	CGT	ATG	GGC	1710
229	Glu	Val	Ile	Ser	Trp	Gly	Ser	Gly	Arg	Gln	Asn	Ser	Pro	Arg	Met	Gly	
230				505						510					515		
232	CAG	CCT	GGA	TCG	GGC	TCC	ATG	CCA	TCA	AGA	TCC	ACT	TCT	CAC	ACT	TCA	1758
233	Gln	Pro	Gly	Ser	Gly	Ser	Met	Pro	Ser	Arg	Ser	Thr	Ser	His	Thr	Ser	
234			520							525					530		
236	GAT	TTC	AAC	CCG	AAT	TCT	GGT	TCA	GAC	CAA	AGA	GTA	GTT	AAT	GGA	GGT	1806
237	Asp	Phe	Asn	Pro	Asn	Ser	Gly	Ser	Asp	Gln	Arg	Val	Val	Asn	Gly	Gly	
238			535					540						545			
240	GTT	CCC	TGG	CCA	TCG	CCT	TGC	CCA	TCT	CCT	TCC	TCT	CGC	CCA	CCT	TCT	1854
241	Val	Pro	Trp	Pro	Ser	Pro	Cys	Pro	Ser	Pro	Ser	Ser	Arg	Pro	Pro	Ser	
242		550					555					560					
244	CGC	TAC	CAG	TCA	GGT	CCC	AAC	TCT	CTT	CCA	CCT	CGG	GCA	GCC	ACC	CCT	1902
245	Arg	Tyr	Gln	Ser	Gly	Pro	Asn	Ser	Leu	Pro	Pro	Arg	Ala	Ala	Thr	Pro	
246	565					570					575					580	
248	ACA	CGG	CCG	CCC	TCC	AGG	CCC	CCC	TCG	CGG	CCA	TCC	AGA	CCC	CCG	TCT	1950
249	Thr	Arg	Pro	Pro	Ser	Arg	Pro	Pro	Ser	Arg	Pro	Ser	Arg	Pro	Pro	Ser	
250				585						590					595		
252	CAC	CCC	TCT	GCT	CAT	GGT	TCT	CCA	GCT	CCT	GTC	TCT	ACT	ATG	CCT	AAA	1998
253	His	Pro	Ser	Ala	His	Gly	Ser	Pro	Ala	Pro	Val	Ser	Thr	Met	Pro	Lys	
254			600							605					610		
256	CGC	ATG	TCT	TCA	GAA	GGG	CCT	CCA	AGG	ATG	TCC	CCA	AAG	GCC	CAG	CGA	2046
257	Arg	Met	Ser	Ser	Glu	Gly	Pro	Pro	Arg	Met	Ser	Pro	Lys	Ala	Gln	Arg	
258			615					620							625		
260	CAT	CCT	CGA	AAT	CAC	AGA	GTT	TCT	GCT	GGG	AGG	GGT	TCC	ATA	TCC	AGT	2094
261	His	Pro	Arg	Asn	His	Arg	Val	Ser	Ala	Gly	Arg	Gly	Ser	Ile	Ser	Ser	
262		630					635					640					
264	GGC	CTA	GAA	TTT	GTA	TCC	CAC	AAC	CCA	CCC	AGT	GAA	GCA	GCT	ACT	CCT	2142
265	Gly	Leu	Glu	Phe	Val	Ser	His	Asn	Pro	Pro	Ser	Glu	Ala	Ala	Thr	Pro	
266	645					650					655					660	
268	CCA	GTA	GCA	AGG	ACC	AGT	CCC	TCG	GGG	GGA	ACG	TGG	TCA	TCA	GTG	GTC	2190
269	Pro	Val	Ala	Arg	Thr	Ser	Pro	Ser	Gly	Gly	Thr	Trp	Ser	Ser	Val	Val	

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270		665		670		675		
272	AGT GGG GTT CCA AGA TTA TCC CCT AAA ACT CAT AGA CCC AGG TCT CCC							2238
273	Ser Gly Val Pro Arg Leu Ser Pro Lys Thr His Arg Pro Arg Ser Pro							
274		680		685		690		
276	AGA CAG AAC AGT ATT GGA AAT ACC CCC AGT GGG CCA GTT CTT GCT TCT							2286
277	Arg Gln Asn Ser Ile Gly Asn Thr Pro Ser Gly Pro Val Leu Ala Ser							
278		695		700		705		
280	CCC CAA GCT GGT ATT ATT CCA ACT GAA GCT GTT GCC ATG CCT ATT CCA							2334
281	Pro Gln Ala Gly Ile Ile Pro Thr Glu Ala Val Ala Met Pro Ile Pro							
282		710		715		720		
284	GCT GCA TCT CCT ACG CCT GCT AGT CCT GCA TCG AAC AGA GCT GTT ACC							2382
285	Ala Ala Ser Pro Thr Pro Ala Ser Pro Ala Ser Asn Arg Ala Val Thr							
286	725		730		735		740	
288	CCT TCT AGT GAG GCT AAA GAT TCC AGG CTT CAA GAT CAG AGG CAG AAC							2430
289	Pro Ser Ser Glu Ala Lys Asp Ser Arg Leu Gln Asp Gln Arg Gln Asn							
290		745		750		755		
292	TCT CCT GCA GGG AAT AAA GAA AAT ATT AAA CCC AAT GAA ACA TCA CCT							2478
293	Ser Pro Ala Gly Asn Lys Glu Asn Ile Lys Pro Asn Glu Thr Ser Pro							
294		760		765		770		
296	AGC TTC TCA AAA GCT GAA AAC AAA GGT ATA TCA CCA GTT GTT TCT GAA							2526
297	Ser Phe Ser Lys Ala Glu Asn Lys Gly Ile Ser Pro Val Val Ser Glu							
298		775		780		785		
300	CAT AGA AAA CAG ATT GAT GAT TTA AAG AAA TTT AAG AAT GAT TTT AGG							2574
301	His Arg Lys Gln Ile Asp Asp Leu Lys Lys Phe Lys Asn Asp Phe Arg							
302		790		795		800		
304	TTA CAG CCA AGT TCT ACT TCT GAA TCT ATG GAT CAA CTA CTA AAC AAA							2622
305	Leu Gln Pro Ser Ser Thr Ser Glu Ser Met Asp Gln Leu Leu Asn Lys							
306	805		810		815		820	
308	AAT AGA GAG GGA GAA AAA TCA AGA GAT TTG ATC AAA GAC AAA ATT GAA							2670
309	Asn Arg Glu Gly Glu Lys Ser Arg Asp Leu Ile Lys Asp Lys Ile Glu							
310		825		830		835		
312	CCA AGT GCT AAG GAT TCT TTC ATT GAA AAT AGC AGC AGC AAC TGT ACC							2718
313	Pro Ser Ala Lys Asp Ser Phe Ile Glu Asn Ser Ser Ser Asn Cys Thr							
314		840		845		850		
316	AGT GGC AGC AGC AAG CCG AAT AGC CCC AGC ATT TCC CCT TCA ATA CTT							2766
317	Ser Gly Ser Ser Lys Pro Asn Ser Pro Ser Ile Ser Pro Ser Ile Leu							
318		855		860		865		
320	AGT AAC ACG GAG CAC AAG AGG GGA CCT GAG GTC ACT TCC CAA GGG GTT							2814
321	Ser Asn Thr Glu His Lys Arg Gly Pro Glu Val Thr Ser Gln Gly Val							
322		870		875		880		
324	CAG ACT TCC AGC CCA GCA TGT AAA CAA GAG AAA GAC GAT AAG GAA GAG							2862
325	Gln Thr Ser Ser Pro Ala Cys Lys Gln Glu Lys Asp Asp Lys Glu Glu							
326	885		890		895		900	
328	AAG AAA GAC GCA GCT GAG CAA GTT AGG AAA TCA ACA TTG AAT CCC AAT							2910
329	Lys Lys Asp Ala Ala Glu Gln Val Arg Lys Ser Thr Leu Asn Pro Asn							
330		905		910		915		
332	GCA AAG GAG TTC AAC CCA CGT TCC TTC TCT CAG CCA AAG CCT TCT ACT							2958
333	Ala Lys Glu Phe Asn Pro Arg Ser Phe Ser Gln Pro Lys Pro Ser Thr							
334		920		925		930		

VERIFICATION SUMMARY

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L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:30 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:33 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1)(vi)